

DS90
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/900,038A

DATE: 10/15/2001
TIME: 13:34:08

Input Set : A:\766.53 Sequence Listing.txt
Output Set: N:\CRF3\10152001\I900038A.raw

3 <110> APPLICANT: Miyake, Katsuhide
4 Watanabe, Masaki
5 Iijima, Shinji
7 <120> TITLE OF INVENTION: Beta 1,3-galactosyltransferase and DNA encoding the same
9 <130> FILE REFERENCE: 766.53
11 <140> CURRENT APPLICATION NUMBER: US 09/900,038A
C--> 12 <141> CURRENT FILING DATE: 2001-09-21
14 <150> PRIOR APPLICATION NUMBER: JP 2001-392
15 <151> PRIOR FILING DATE: 2001-01-05
17 <160> NUMBER OF SEQ ID NOS: 8
19 <170> SOFTWARE: PatentIn Ver. 2.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 313
23 <212> TYPE: PRT
24 <213> ORGANISM: Streptococcus agalactiae Type Ib
W--> 25 <400> SEQUENCE: 1
26 Met Asn Tyr Ser Ile Ile Met Ser Val Tyr Asn Glu Pro Leu Asn Tyr
27 1 5 10 15
29 Val Arg Asp Ser Val Glu Ser Ile Leu Asn Gln Thr Leu Thr Asp Phe
30 20 25 30
32 Glu Phe Ile Ile Val Ile Asp Asn Pro Ser Arg Gly Asp Leu Lys Gln
33 35 40 45
35 Phe Leu Thr Glu Tyr Ser Val Val Asp Asn Arg Ile Lys Ile Leu Leu
36 50 55 60
38 Asn Glu Glu Asn Ile Gly Leu Ala Ser Ser Leu Asn Lys Ala Val Lys
39 65 70 75 80
41 Ile Ser Lys Gly Glu Tyr Ile Phe Arg Met Asp Ala Asp Asp Ile Ser
42 85 90 95
44 Tyr Pro Ser Arg Phe Asp Lys Gln Ile Arg Phe Met Glu Glu Asn Ser
45 100 105 110
47 Leu Asp Phe Ser Ala Thr Leu Ile Glu Leu Ile Asp Gln Lys Gly Asn
48 115 120 125
50 Leu Val Tyr Lys Gln Arg Glu Ser Asn Lys Ile Tyr Leu Thr Asn Asp
51 130 135 140
53 Ile Arg Lys Met Leu Leu Asn Arg Ser Ile Leu Ala His Pro Thr Trp
54 145 150 155 160
56 Cys Val Lys Lys Val Phe Asp Lys Leu Met Gly Tyr Arg Asp Leu
57 165 170 175
59 Val Pro Val Glu Asp Tyr Asp Phe Ala Ile Arg Gly Ala Leu Ala Asp
60 180 185 190
62 Phe Lys Ile Gly Leu Leu Asn Lys Val Leu Leu Gln Tyr Arg Leu Asn
63 195 200 205
65 Glu Asn Gly Ile Ser Gln Thr Asn Lys Phe Lys Gln Tyr Ile Tyr Ser
66 210 215 220
68 Ala Ile Leu Gln Asp Phe Tyr Lys Glu Lys Ser Tyr Ile Asp Ile Thr
69 225 230 235 240
71 Lys Ile Thr Asn Tyr Phe Gln Glu Tyr Val Ile Lys Lys Arg Tyr Thr

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72	245	250	255
74	Gln Gln Glu Leu Ser Lys Tyr Phe Glu Leu Lys Ser Thr Pro Ser Ile		
75	260	265	270
77	Thr Ile Arg Lys Leu Tyr Ile Cys Leu Tyr Leu Tyr Phe Lys Ser Pro		
78	275	280	285
80	Leu Val Arg Arg Leu Leu Ile Asn Asp Ile Asn Ile Leu Val Leu Lys		
81	290	295	300
83	Leu Phe Gly Gly Glu Lys Gln Ser Asp		
84	305	310	
86	<210> SEQ ID NO: 2		
87	<211> LENGTH: 939		
88	<212> TYPE: DNA		
89	<213> ORGANISM: Streptococcus agalactiae Type Ib		
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92	Met Asn Tyr Ser Ile Ile Met Ser Val Tyr Asn Glu Pro Leu Asn Tyr		
93	1 5 10 15		
95	gtg aga gat tca gta gaa tct ata tta aat caa acg ctt act gat ttt	96	
96	Val Arg Asp Ser Val Glu Ser Ile Leu Asn Gln Thr Leu Thr Asp Phe		
97	20 25 30		
99	gag ttc ata att gtc att gat aat cca agt aga ggt gat tta aag caa	144	
100	Glu Phe Ile Ile Val Ile Asp Asn Pro Ser Arg Gly Asp Leu Lys Gln		
101	35 40 45		
103	tcc tta aca gaa tat tca gtt gta gat aat aga ata aaa atc ttg ctt	192	
104	Phe Leu Thr Glu Tyr Ser Val Val Asp Asn Arg Ile Lys Ile Leu Leu		
105	50 55 60		
107	aat gaa gaa aat att ggt tta gca tca agt ttg aac aaa gcg gtg aaa	240	
108	Asn Glu Glu Asn Ile Gly Leu Ala Ser Ser Leu Asn Lys Ala Val Lys		
109	65 70 75 80		
111	att tct aag gga gaa tat att ttt aga atg gat gct gat gat att tca	288	
112	Ile Ser Lys Gly Glu Tyr Ile Phe Arg Met Asp Ala Asp Asp Ile Ser		
113	85 90 95		
115	tat cca agt aga ttt gat aag caa att cgt ttt atg gag gaa aat tca	336	
116	Tyr Pro Ser Arg Phe Asp Lys Gln Ile Arg Phe Met Glu Glu Asn Ser		
117	100 105 110		
119	ttg gat ttc tca gca act cta ata gaa ttg ata gac caa aaa gga aat	384	
120	Leu Asp Phe Ser Ala Thr Leu Ile Glu Leu Ile Asp Gln Lys Gly Asn		
121	115 120 125		
123	tta gta tat aaa caa cga gaa agt aat aaa ata tac tta act aat gat	432	
124	Leu Val Tyr Lys Gln Arg Glu Ser Asn Lys Ile Tyr Leu Thr Asn Asp		
125	130 135 140		
127	ata cgg aag atg tta ttg aat aga tct ata ctt gcc cac cca acg tgg	480	
128	Ile Arg Lys Met Leu Leu Asn Arg Ser Ile Leu Ala His Pro Thr Trp		
129	145 150 155 160		
131	tgc gta aaa aag aaa gtt ttc gat aag tta atg gga tat aga gat tta	528	
132	Cys Val Lys Lys Val Phe Asp Lys Leu Met Gly Tyr Arg Asp Leu		
133	165 170 175		
135	gta cct gtt gaa gat tat gat ttt gca ata aga gga gct ctg gct gat	576	
136	Val Pro Val Glu Asp Tyr Asp Phe Ala Ile Arg Gly Ala Leu Ala Asp		

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137 180 185 190
 139 ttc aaa atc ggc tta ctc aat aaa gta ctt tta cag tat aga tta aac 624
 140 Phe Lys Ile Gly Leu Leu Asn Lys Val Leu Leu Gln Tyr Arg Leu Asn
 141 195 200 205
 143 gag aat gga ata tca caa acc aat aag ttt aag caa tat att tac tca 672
 144 Glu Asn Gly Ile Ser Gln Thr Asn Lys Phe Lys Gln Tyr Ile Tyr Ser
 145 210 215 220
 147 gct att tta caa gat ttt tat aaa gaa aaa tct tat att gat atc aca 720
 148 Ala Ile Leu Gln Asp Phe Tyr Lys Glu Lys Ser Tyr Ile Asp Ile Thr
 149 225 230 235 240
 151 aaa att act aat tac ttt caa gag tat gtg ata aag aaa cgc tat act 768
 152 Lys Ile Thr Asn Tyr Phe Gln Glu Tyr Val Ile Lys Lys Arg Tyr Thr
 153 245 250 255
 155 cag caa gag ctc tct aaa tat ttt gag cta aaa tct acc cct agt att 816
 156 Gln Gln Glu Leu Ser Lys Tyr Phe Glu Leu Lys Ser Thr Pro Ser Ile
 157 260 265 270
 159 act att aga aaa cta tat att tgt tta tat tta tac ttt aag tct ccc 864
 160 Thr Ile Arg Lys Leu Tyr Ile Cys Leu Tyr Leu Tyr Phe Lys Ser Pro
 161 275 280 285
 163 ttg gtt agg agg tta tta ata aat gat att aat att tta gta ctg aaa 912
 164 Leu Val Arg Arg Leu Leu Ile Asn Asp Ile Asn Ile Leu Val Leu Lys
 165 290 295 300
 167 ttg ttt gga gga gag aaa caa agt gac
 168 Leu Phe Gly Gly Glu Lys Gln Ser Asp
 169 305 310
 172 <210> SEQ ID NO: 3
 173 <211> LENGTH: 6865
 174 <212> TYPE: DNA
 175 <213> ORGANISM: Streptococcus agalactiae type Ib
 177 <220> FEATURE:
 178 <221> NAME/KEY: CDS
 179 <222> LOCATION: (617)..(1789)
 181 <220> FEATURE:
 182 <221> NAME/KEY: CDS
 183 <222> LOCATION: (1816)..(2262)
 185 <220> FEATURE:
 186 <221> NAME/KEY: CDS
 187 <222> LOCATION: (2265)..(2744)
 189 <220> FEATURE:
 190 <221> NAME/KEY: CDS
 191 <222> LOCATION: (2843)..(3979)
 193 <220> FEATURE:
 194 <221> NAME/KEY: CDS
 195 <222> LOCATION: (3982)..(4953)
 197 <220> FEATURE:
 198 <221> NAME/KEY: CDS
 199 <222> LOCATION: (5009)..(5947)
 201 <400> SEQUENCE: 3
 202 agatcttggatattatctgtgaaaccaaatacgatggtcgttccttcagg 60

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204	gaaaagtacca	ccaaatccaa	cagcattact	tcagaacgct	tatTTtaata	agatgattga	120
206	agcttattaa	aatatatttg	attatattat	catcgatact	ccaccttattg	gttagttgt	180
208	tgtatGCCGCA	ataatcgcta	atgcTTGCGA	tggtttatt	ttagtaaccc	aagcaggtag	240
210	aataaaaacgt	aattatgttg	aaaaagcaa	agaacagatg	gaacaaagtg	gttcaaagg	300
212	cttaggtatt	attcttaata	aagttaatga	atctgttgct	acttacggcg	attatggaaa	360
214	ttacggaaaa	agggatagaa	aaaggaagta	aggggcttt	gtattgaaag	aaaaagaaaa	420
216	tatacAAAAG	attattatag	cgtatgattca	aaccgttGtg	gtttattttt	ctgcaagttt	480
218	gacattaaca	ttaattactc	ccaactttaa	aagcaataaa	gatttatgtt	ttttcttatt	540
220	gatacattat	attgtctttt	atctttctga	tttttacaga	gacttttGga	gtcgTggcta	600
222	tcttgaagag	tttaaaa	atg gta ttg	aaa tac agc	ttt tac tat	att ttc ata	652
223			Met Val Leu Lys	Tyr Ser Phe	Tyr Tyr Ile	Phe Ile	
224		1		5		10	
226	tca agt tca	tta ttt	ttt att	tct aaa aac	tct ttt aca	acg aca cga	700
227	Ser Ser Ser	Leu Phe Phe	Ile Ser Lys Asn	Ser Phe Thr	Thr Thr Arg		
228	15		20		25		
230	ctt tcc ttt	ttt act ttt	att gct atg	aat tcg att tta	tta tat cta		748
231	Leu Ser Phe	Phe Thr Phe	Ile Ala Met	Asn Ser Ile	Leu Tyr Leu		
232	30		35		40		
234	ttg aat tca	ttt tta	aaa tat tat	cga aaa tat	tct tac gct	aag ttt	796
235	Leu Asn Ser	Phe Leu Lys	Tyr Tyr Arg	Lys Tyr Ser	Tyr Ala Lys	Phe	
236	45		50		55	60	
238	tca cga gat	acc aaa gtt	gtt ttg	ata acg aat	aag gat tct	tta tca	844
239	Ser Arg Asp	Thr Lys Val	Val Leu Ile	Thr Asn Lys	Asp Ser	Leu Ser	
240	65		70		75		
242	aaa atg acc	ttt agg aat	aaa tac gac	cat aat tat	atc gct gtc	tgt	892
243	Lys Met Thr	Phe Arg Asn	Lys Tyr Asp	His Asn Tyr	Ile Ala Val	Cys	
244	80		85		90		
246	atc ttg gat	tcc tct gaa	aag gat tgt	tat gat ttg	aaa cat aac	tcg	940
247	Ile Leu Asp	Ser Ser Glu	Lys Asp Cys	Tyr Asp Leu	Lys His	Asn Ser	
248	95		100		105		
250	tta agg ata	ata aac aaa	gat gct ctt	act tca gag	tta acc tgc	tta	988
251	Leu Arg Ile	Ile Asn Lys	Asp Ala	Leu Thr Ser	Glu Leu	Thr Cys	Leu
252	110		115		120		
254	act gtt gat	caa gct ttt	att aac ata	ccc att gaa tta	ttt ggt	aaa	1036
255	Thr Val Asp	Gln Ala Phe	Ile Asn Ile	Pro Ile Glu	Leu Phe	Gly Lys	
256	125		130		135	140	
258	tac caa ata	caa gat att	att aat gac	att gaa gca	atg gga	gtg att	1084
259	Tyr Gln Ile	Gln Asp Ile	Ile Asn Asp	Ile Glu Ala	Met Gly	Val Ile	
260	145		150		155		
262	gtc aat gtt	aat gta gag	gca ctt agc	ttt gat aat	ata gga	gaa aag	1132
263	Val Asn Val	Asn Val Glu	Ala Leu Ser	Phe Asp Asn	Ile Gly	Glu Lys	
264	160		165		170		
266	cga atc caa	act ttt gaa	gga tat	agt gtt att	aca tat	tct atg aaa	1180
267	Arg Ile Gln	Thr Phe Glu	Gly Tyr Ser	Val Ile Thr	Tyr Ser	Met Lys	
268	175		180		185		
270	tcc tat aaa	tat agt cac	ctt ata gca	aaa cga	ttt ttg	gat atc atg	1228
271	Phe Tyr Lys	Tyr Ser His	Leu Ile Ala	Lys Arg Phe	Leu Asp	Ile Met	
272	190		195		200		
274	ggt gct att	ata ggt ttg	ctc ata	tgt ggc	att gtg	gca att ttt cta	1276

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275	Gly Ala Ile Ile Gly Leu Leu Ile Cys Gly Ile Val Ala Ile Phe Leu			
276	205	210	215	220
278	gtt ccg caa atc aga aaa gat ggt gga ccg gct atc ttt tct caa aat			1324
279	Val Pro Gln Ile Arg Lys Asp Gly Gly Pro Ala Ile Phe Ser Gln Asn			
280	225	230	235	
282	aga gta ggt cgt aat ggt agg att ttt aga ttc tat aaa ttc aga tca			1372
283	Arg Val Gly Arg Asn Gly Arg Ile Phe Arg Phe Tyr Lys Phe Arg Ser			
284	240	245	250	
286	atg cga gta gat gca gaa caa att aag aaa gat tta tta gtt cac aat			1420
287	Met Arg Val Asp Ala Glu Gln Ile Lys Lys Asp Leu Leu Val His Asn			
288	255	260	265	
290	caa atg acg ggg cta atg ttt aag tta gac gat gat cct aga att act			1468
291	Gln Met Thr Gly Leu Met Phe Lys Leu Asp Asp Asp Pro Arg Ile Thr			
292	270	275	280	
294	aaa ata gga aaa ttt att cga aaa aca agc ata gat gag ttg cct caa			1516
295	Lys Ile Gly Lys Phe Ile Arg Lys Thr Ser Ile Asp Glu Leu Pro Gln			
296	285	290	295	300
298	tcc tat aat gtt tta aaa ggt gat atg agt tta gta gga aca cgc cct			1564
299	Phe Tyr Asn Val Leu Lys Gly Asp Met Ser Leu Val Gly Thr Arg Pro			
300	305	310	315	
302	ccc aca gtt gat gaa tat gaa aag tat aat tca acg cag aag cga cgc			1612
303	Pro Thr Val Asp Glu Tyr Glu Lys Tyr Asn Ser Thr Gln Lys Arg Arg			
304	320	325	330	
306	ctt agt ttt aag cca gga atc act ggt ttg tgg caa ata tct ggt aga			1660
307	Leu Ser Phe Lys Pro Gly Ile Thr Gly Leu Trp Gln Ile Ser Gly Arg			
308	335	340	345	
310	aat aat att act gat ttt gat gaa atc gta aag tta gat gtt caa tat			1708
311	Asn Asn Ile Thr Asp Phe Asp Glu Ile Val Lys Leu Asp Val Gln Tyr			
312	350	355	360	
314	atc aat gaa tgg tct att tgg tca gat att aag att att ctc cta acg			1756
315	Ile Asn Glu Trp Ser Ile Trp Ser Asp Ile Lys Ile Ile Leu Leu Thr			
316	365	370	375	380
318	cta aag gta gtt tta ctc ggg aca gga gct aag taaaggtaag gtttggaaagg	1809		
319	Leu Lys Val Val Leu Leu Gly Thr Gly Ala Lys			
320	385	390		
322	aatata atg aaa att tgt ctg gtt ggt tca agt ggt ggt cac cta gca			1857
323	Met Lys Ile Cys Leu Val Gly Ser Ser Gly Gly His Leu Ala			
324	395	400	405	
326	cac ttg aac ctt ttg aaa ccc att tgg gaa aaa gaa gat agg ttt tgg			1905
327	His Leu Asn Leu Leu Lys Pro Ile Trp Glu Lys Glu Asp Arg Phe Trp			
328	410	415	420	
330	gta act ttt gat aaa gaa gat gct agg agt att cta aga gaa gag att			1953
331	Val Thr Phe Asp Lys Glu Asp Ala Arg Ser Ile Leu Arg Glu Glu Ile			
332	425	430	435	
334	gta tat cat tgc ttc ttt cca aca aac cgt aat gtc aaa aac ttg gta			2001
335	Val Tyr His Cys Phe Phe Pro Thr Asn Arg Asn Val Lys Asn Leu Val			
336	440	445	450	
338	aaa aat act att cta gct ttt aag gtc ctt aga aaa gaa aga cca gat			2049
339	Lys Asn Thr Ile Leu Ala Phe Lys Val Leu Arg Lys Glu Arg Pro Asp			

VERIFICATION SUMMARY
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L:25 M:283 W: Missing Blank Line separator, <400> field identifier
L:90 M:283 W: Missing Blank Line separator, <400> field identifier
L:698 M:283 W: Missing Blank Line separator, <220> field identifier
L:700 M:283 W: Missing Blank Line separator, <400> field identifier
L:709 M:283 W: Missing Blank Line separator, <220> field identifier
L:711 M:283 W: Missing Blank Line separator, <400> field identifier
L:719 M:283 W: Missing Blank Line separator, <220> field identifier
L:721 M:283 W: Missing Blank Line separator, <400> field identifier
L:729 M:283 W: Missing Blank Line separator, <220> field identifier
L:731 M:283 W: Missing Blank Line separator, <400> field identifier
L:739 M:283 W: Missing Blank Line separator, <220> field identifier
L:741 M:283 W: Missing Blank Line separator, <400> field identifier